1632

RAW SEQUENCE LISTING DATE: 06/09/2000
PATENT APPLICATION: US/09/494,096 TIME: 12:33:29

Input Set : A:\Hs102c21.app
Output Set: N:\CRF3\06082000\I494096.raw

ENTERED

<110> APPLICANT: Bannon, Gary A.
Burks Jr., A. Wesley
Sampson, Hugh A.
Sosin, Howard B.
<120> TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions to Allergy
<130> FILE REFERENCE: HS 102 CIP (2)
<140> CURRENT APPLICATION NUMBER: 09/494,096
<141> CURRENT FILING DATE: 2000-01-28
<150> PRIOR APPLICATION NUMBER: 09/141,220
<151> PRIOR FILING DATE: 1998-08-27
<150> PRIOR APPLICATION NUMBER: 09/240,557
<151> PRIOR FILING DATE: 1999-01-29
<150> PRIOR APPLICATION NUMBER: 09/241,101
<151> PRIOR FILING DATE: 1999-01-29
<150> PRIOR APPLICATION NUMBER: 09/248,673
<151> PRIOR FILING DATE: 1999-02-11
<150> PRIOR APPLICATION NUMBER: 60/073,283
<151> PRIOR FILING DATE: 1998-01-29
<150> PRIOR APPLICATION NUMBER: 60/074,590
<151> PRIOR FILING DATE: 1998-02-13
<150> PRIOR APPLICATION NUMBER: 60/074,624
<151> PRIOR FILING DATE: 1998-02-13
<150> PRIOR APPLICATION NUMBER: 09/248,674
<151> PRIOR FILING DATE: 1999-02-11
<150> PRIOR APPLICATION NUMBER: 60/122,566
<151> PRIOR FILING DATE: 1999-03-02
<160> NUMBER OF SEQ ID NOS: 6
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO: 1
<211> LENGTH: 626
<212> TYPE: PRT
<213> ORGANISM: Arachis hypogaea
<400> SEQUENCE: 1

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Leu Ala Ser Val Ser Ala Thr His Ala Lys Ser Ser Pro Tyr Gln Lys
            20                  25                  30
Lys Thr Glu Asn Pro Cys Ala Gln Arg Cys Leu Gln Ser Cys Gln Gln
        35                  40                  45
Glu Pro Asp Asp Leu Lys Gln Lys Ala Cys Glu Ser Arg Cys Thr Lys
    50                  55                  60
Leu Glu Tyr Asp Pro Arg Leu Val Tyr Asp Pro Arg Gly His Thr Gly
65                  70                  75                  80
Thr Thr Asn Gln Arg Ser Pro Pro Gly Glu Arg Thr Arg Gly Arg Gln
                85                  90                  95
Pro Gly Asp Tyr Asp Asp Asp Arg Arg Gln Pro Arg Arg Glu Glu Gly
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72              100                 105                 110
74 Gly Arg Trp Gly Pro Ala Gly Pro Arg Glu Arg Glu Arg Glu Glu Asp
75          115                 120                 125
77 Trp Arg Gln Pro Arg Glu Asp Trp Arg Arg Pro Ser His Gln Gln Pro
78      130                 135                 140
80 Arg Lys Ile Arg Pro Glu Gly Arg Glu Gly Glu Gln Glu Trp Gly Thr
81 145                 150                 155                 160
83 Pro Gly Ser His Val Arg Glu Glu Thr Ser Arg Asn Asn Pro Phe Tyr
84                  165                 170                 175
86 Phe Pro Ser Arg Arg Phe Ser Thr Arg Tyr Gly Asn Gln Asn Gly Arg
87              180                 185                 190
89 Ile Arg Val Leu Gln Arg Phe Asp Gln Arg Ser Arg Gln Phe Gln Asn
90          195                 200                 205
92 Leu Gln Asn His Arg Ile Val Gln Ile Glu Ala Lys Pro Asn Thr Leu
93      210                 215                 220
95 Val Leu Pro Lys His Ala Asp Ala Asp Asn Ile Leu Val Ile Gln Gln
96 225                 230                 235                 240
98 Gly Gln Ala Thr Val Thr Val Ala Asn Gly Asn Asn Arg Lys Ser Phe
99                  245                 250                 255
101 Asn Leu Asp Glu Gly His Ala Leu Arg Ile Pro Ser Gly Phe Ile Ser
102             260                 265                 270
104 Tyr Ile Leu Asn Arg His Asp Asn Gln Asn Leu Arg Val Ala Lys Ile
105         275                 280                 285
107 Ser Met Pro Val Asn Thr Pro Gly Gln Phe Glu Asp Phe Phe Pro Ala
108     290                 295                 300
110 Ser Ser Arg Asp Gln Ser Ser Tyr Leu Gln Glu Phe Ser Arg Asn Thr
111 305                 310                 315                 320
113 Leu Glu Ala Ala Phe Asn Ala Glu Phe Asn Glu Ile Arg Arg Val Leu
114                 325                 330                 335
116 Leu Glu Glu Asn Ala Gly Gly Glu Gln Glu Glu Arg Gly Gln Arg Arg
117             340                 345                 350
119 Trp Ser Thr Arg Ser Ser Glu Asn Asn Glu Gly Val Ile Val Lys Val
120         355                 360                 365
122 Ser Lys Glu His Val Glu Glu Leu Thr Lys His Ala Lys Ser Val Ser
123     370                 375                 380
125 Lys Lys Gly Ser Glu Glu Glu Gly Asp Ile Thr Asn Pro Ile Asn Leu
126 385                 390                 395                 400
128 Arg Glu Gly Glu Pro Asp Leu Ser Asn Asn Phe Gly Lys Leu Phe Glu
129                 405                 410                 415
131 Val Lys Pro Asp Lys Lys Asn Pro Gln Leu Gln Asp Leu Asp Met Met
132             420                 425                 430
134 Leu Thr Cys Val Glu Ile Lys Glu Gly Ala Leu Met Leu Pro His Phe
135         435                 440                 445
137 Asn Ser Lys Ala Met Val Ile Val Val Val Asn Lys Gly Thr Gly Asn
138     450                 455                 460
140 Leu Glu Leu Val Ala Val Arg Lys Glu Gln Gln Gln Arg Gly Arg Arg
141 465                 470                 475                 480
143 Glu Glu Glu Glu Asp Glu Asp Glu Glu Glu Glu Gly Ser Asn Arg Glu
144                 485                 490                 495
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146 Val Arg Arg Tyr Thr Ala Arg Leu Lys Glu Gly Asp Val Phe Ile Met
147             500                 505                 510
149 Pro Ala Ala His Pro Val Ala Ile Asn Ala Ser Ser Glu Leu His Leu
150         515                 520                 525
152 Leu Gly Phe Gly Ile Asn Ala Glu Asn Asn His Arg Ile Phe Leu Ala
153     530                 535                 540
155 Gly Asp Lys Asp Asn Val Ile Asp Gln Ile Glu Lys Gln Ala Lys Asp
156 545                 550                 555                 560
158 Leu Ala Phe Pro Gly Ser Gly Glu Gln Val Glu Lys Leu Ile Lys Asn
159                 565                 570                 575
161 Gln Lys Glu Ser His Phe Val Ser Ala Arg Pro Gln Ser Gln Ser Gln
162             580                 585                 590
164 Ser Pro Ser Ser Pro Glu Lys Glu Ser Pro Glu Lys Glu Asp Gln Glu
165         595                 600                 605
167 Glu Glu Asn Gln Gly Gly Lys Gly Pro Leu Leu Ser Ile Leu Lys Ala
168     610                 615                 620
170 Phe Asn
171 625
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175 <211> LENGTH: 1930
176 <212> TYPE: DNA
177 <213> ORGANISM: Arachis hypogaea
179 <400> SEQUENCE: 2
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181 ggtttctcca ctgatgctgt tgctagggat ccttgtcctg gcttcagttt ctgcaacgca 120
182 tgccaagtca tcaccttacc agaagaaaac agagaacccc tgcgcccaga ggtgcctcca 180
183 gagttgtcaa caggaaccgg atgacttgaa gcaaaaggca tgcgagtctc gctgcaccaa 240
184 gctcgagtat gatcctcgtt gtgtctatga tcctcgagga cacactggca ccaccaacca 300
185 acgttccgct ccaggggagc ggacacgtgg ccgccaaccc ggagactacg atgatgaccg 360
186 ccgtcaaccc cgaagagagg aaggaggccg atggggacca gctggaccga gggagcgtga 420
187 aagagaagaa gactggagac aaccaagaga agattggagg cgaccaagtc atcagcagcc 480
188 acggaaaata aggcccgaag gaagagaagg agaacaagag tggggaacac caggtagcca 540
189 tgtgagggaa gaaacatctc ggaacaaccc tttctacttc ccgtcaaggc ggtttagcac 600
190 ccgctacggg aaccaaaacg gtaggatccg ggtcctgcag aggtttgacc aaaggtcaag 660
191 gcagtttcag aatctccaga atcaccgtat tgtgcagatc gaggccaaac ctaacactct 720
192 tgttcttccc aagcacgctg atgctgataa catccttgtt atccagcaag ggcaagccac 780
193 cgtgaccgta gcaaatggca ataacagaaa gagctttaat cttgacgagg gccatgcact 840
194 cagaatccca tccggtttca tttcctacat cttgaaccgc catgacaacc agaacctcag 900
195 agtagctaaa atctccatgc ccgttaacac acccggccag tttgaggatt tcttcccggc 960
196 gagcagccga gaccaatcat cctacttgca gggcttcagc aggaatacgt tggaggccgc 1020
197 cttcaatgcg gaattcaatg agatacggag ggtgctgtta gaagagaatg caggaggtga 1080
198 gcaagaggag agagggcaga ggcgatggag tactcggagt agtgagaaca atgaaggagt 1140
199 gatagtcaaa gtgtcaaagg agcacgttga agaacttact aagcacgcta aatccgtctc 1200
200 aaagaaaggc tccgaagaag agggagatat caccaaccca atcaacttga gagaaggcga 1260
201 gcccgatctt tctaacaact ttgggaagtt atttgaggtg aagccagaca agaagaaccc 1320
202 ccagcttcag gacctggaca tgatgctcac ctgtgtagag atcaaagaag gagctttgat 1380
203 gctcccacac ttcaactcaa aggccatggt tatcgtcgtc gtcaacaaag gaactggaaa 1440
204 ccttgaactc gtggctgtaa gaaaagagca acaacagagg ggacggcggg aagaagagga 1500
205 ggacgaagac gaagaagagg agggaagtaa cagagaggtg cgtaggtaca cagcgaggtt 1560
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gaaggaaggc gatgtgttca tcatgccagc agctcatcca gtagccatca acgcttcctc 1620
cgaactccat ctgcttggct tcggtatcaa cgctgaaaac aaccacagaa tcttccttgc 1680
aggtgataag gacaatgtga tagaccagat agagaagcaa gcgaaggatt tagcattccc 1740
tgggtcgggt gaacaagttg agaagctcat caaaaaccag aaggaatctc actttgtgag 1800
tgctcgtcct caatctcaat ctcaatctcc gtcgtctcct gagaaagagt ctcctgagaa 1860
agaggatcaa gaggaggaaa accaaggagg gaagggtcca ctcctttcaa ttttgaaggc 1920
ttttaactga 1930

<210> SEQ ID NO: 3
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<212> TYPE: PRT
<213> ORGANISM: Arachis hypogaea
<400> SEQUENCE: 3

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 1               5                  10                  15
Ser Ala Arg Gln Gln Trp Glu Leu Gln Gly Asp Arg Arg Cys Gln Ser
            20                  25                  30
Gln Leu Glu Arg Ala Asn Leu Arg Pro Cys Glu Gln His Leu Met Gln
        35                  40                  45
Lys Ile Gln Arg Asp Glu Asp Ser Tyr Glu Arg Asp Pro Tyr Ser Pro
    50                  55                  60
Ser Gln Asp Pro Tyr Ser Pro Ser Pro Tyr Asp Arg Arg Gly Ala Gly
65                  70                  75                  80
Ser Ser Gln His Gln Glu Arg Cys Cys Asn Glu Leu Asn Glu Phe Glu
                85                  90                  95
Asn Asn Gln Arg Cys Met Cys Glu Ala Leu Gln Gln Ile Met Glu Asn
            100                 105                 110
Gln Ser Asp Arg Leu Gln Gly Arg Gln Gln Glu Gln Gln Phe Lys Arg
        115                 120                 125
Glu Leu Arg Asn Leu Pro Gln Gln Cys Gly Leu Arg Ala Pro Gln Arg
    130                 135                 140
Cys Asp Leu Asp Val Glu Ser Gly Gly Arg Asp Arg Tyr
145                 150                 155
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<212> TYPE: DNA
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cagtgggaac tccaaggaga cagaagatgc cagagccagc tcgagagggc gaacctgagg 120
ccctgcgagc aacatctcat gcagaagatc caacgtgacg aggattcata tgaacgggac 180
ccgtacagcc ctagtcagga tccgtacagc cctagtccat atgatcggag aggcgctgga 240
tcctctcagc accaagagag gtgttgcaat gagctgaacg agtttgagaa caaccaaagg 300
tgcatgtgcg aggcattgca acagatcatg gagaaccaga gcgataggtt gcaggggagg 360
caacaggagc aacagttcaa gagggagctc aggaacttgc ctcaacagtg cggccttagg 420
gcaccacagc gttgcgactt ggacgtcgaa agtggcggca gagacagata ctaa       474
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<211> LENGTH: 510
<212> TYPE: PRT
<213> ORGANISM: Arachis hypogaea

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<400> SEQUENCE: 5

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Ile Ser Phe Arg Gln Gln Pro Glu Glu Asn Ala Cys Gln Phe Gln Arg
 1               5                  10                  15
Leu Asn Ala Gln Arg Pro Asp Asn Arg Ile Glu Ser Glu Gly Gly Tyr
            20                  25                  30
Ile Glu Thr Trp Asn Pro Asn Asn Gln Glu Phe Glu Cys Ala Gly Val
        35                  40                  45
Ala Leu Ser Arg Leu Val Leu Arg Arg Asn Ala Leu Arg Arg Pro Phe
    50                  55                  60
Tyr Ser Asn Ala Pro Gln Glu Ile Phe Ile Gln Gln Gly Arg Gly Tyr
65                  70                  75                  80
Phe Gly Leu Ile Phe Pro Gly Cys Pro Arg His Tyr Glu Glu Pro His
                85                  90                  95
Thr Gln Gly Arg Arg Ser Gln Ser Gln Arg Pro Pro Arg Arg Leu Gln
            100                 105                 110
Gly Glu Asp Gln Ser Gln Gln Gln Arg Asp Ser His Gln Lys Val His
        115                 120                 125
Arg Phe Asp Glu Gly Asp Leu Ile Ala Val Pro Thr Gly Val Ala Phe
    130                 135                 140
Trp Leu Tyr Asn Asp His Asp Thr Asp Val Val Ala Val Ser Leu Thr
145                 150                 155                 160
Asp Thr Asn Asn Asn Asp Asn Gln Leu Asp Gln Phe Pro Arg Arg Phe
                165                 170                 175
Asn Leu Ala Gly Asn Thr Glu Gln Glu Phe Leu Arg Tyr Gln Gln Gln
            180                 185                 190
Ser Arg Gln Ser Arg Arg Arg Ser Leu Pro Tyr Ser Pro Tyr Ser Pro
        195                 200                 205
Gln Ser Gln Pro Arg Gln Glu Glu Arg Glu Phe Ser Pro Arg Gly Gln
    210                 215                 220
His Ser Arg Arg Glu Arg Ala Gly Gln Glu Glu Glu Asn Glu Gly Gly
225                 230                 235                 240
Asn Ile Phe Ser Gly Phe Thr Pro Glu Phe Leu Glu Gln Ala Phe Gln
                245                 250                 255
Val Asp Asp Arg Gln Ile Val Gln Asn Leu Arg Gly Glu Thr Glu Ser
            260                 265                 270
Glu Glu Glu Glu Gly Ala Ile Val Thr Val Arg Gly Gly Leu Arg Ile Leu
        275                 280                 285
Ser Pro Asp Arg Lys Arg Arg Ala Asp Glu Glu Glu Glu Tyr Asp Glu
    290                 295                 300
Asp Glu Tyr Glu Tyr Asp Glu Glu Asp Arg Arg Arg Gly Arg Gly Ser
305                 310                 315                 320
Arg Gly Arg Gly Asn Gly Ile Glu Glu Thr Ile Cys Thr Ala Ser Ala
                325                 330                 335
Lys Lys Asn Ile Gly Arg Asn Arg Ser Pro Asp Ile Tyr Asn Pro Gln
            340                 345                 350
Ala Gly Ser Leu Lys Thr Ala Asn Asp Leu Asn Leu Leu Ile Leu Arg
        355                 360                 365
Trp Leu Gly Leu Ser Ala Glu Tyr Gly Asn Leu Tyr Arg Asn Ala Leu
    370                 375                 380
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